NCBI Blast 2 Sequences results

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.14 [May-07-2006]
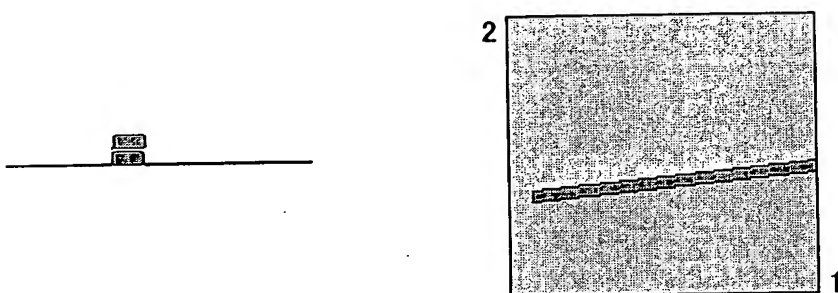
Match: 1   Mismatch: -2   gap open: 5   gap extension: 2
x_dropoff: 50   expect: 10.000   wordsize: 11   Filter ☑   View option Standard ▾
Masking character option X for protein, n for nucleotide ▾   Masking color option Black ▾
☐ Show CDS translation   Align

Sequence 1: lcl|1_seq_1
Length = 459 (1 .. 459)

Sequence 2: lcl|2_seq_2
Length = 4258 (1 .. 4258)

NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.


```
Score =  812 bits (422),  Expect = 0.0
Identities = 422/422 (100%),  Gaps = 0/422 (0%)
Strand=Plus/Plus

Query  38    GGAACATCGAGGACATCTACCGCTGCCAGAAGGCCTTCGTGAAGGCCCTGGAGCAGAGGT  97
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1512  GGAACATCGAGGACATCTACCGCTGCCAGAAGGCCTTCGTGAAGGCCCTGGAGCAGAGGT  1571

Query  98    TCAACCGCGAGCGCCCACACCTGAGCGAGCTGGGTGCCTGCTTCCTGGAGCATCAAGCCG  157
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1572  TCAACCGCGAGCGCCCACACCTGAGCGAGCTGGGTGCCTGCTTCCTGGAGCATCAAGCCG  1631

Query  158   ACTTCCAGATCTACTCGGAGTACTGCAATAACCACCCCAACGCCTGCGTGGAGCTCTCCC  217
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1632  ACTTCCAGATCTACTCGGAGTACTGCAATAACCACCCCAACGCCTGCGTGGAGCTCTCCC  1691

Query  218   GGCTCACCAAGCTCAGCAAGTACGTGTACTTCTTCGAGGCCTGCCGGCTGCTGCAGAAGA  277
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1692  GGCTCACCAAGCTCAGCAAGTACGTGTACTTCTTCGAGGCCTGCCGGCTGCTGCAGAAGA  1751

Query  278   TGATTGACATCTCCCTGGATGGCTTCCTGCTGACTCCGGTGCAGAAGATCTGCAAGTACC  337
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1752  TGATTGACATCTCCCTGGATGGCTTCCTGCTGACTCCGGTGCAGAAGATCTGCAAGTACC  1811
```

```
Query  338   CTCTGCAGCTGGCCGAGCTGCTCAAATACACGCACCCCCAGCACAGGGACTTCAAGGATG   397
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1812  CTCTGCAGCTGGCCGAGCTGCTCAAATACACGCACCCCCAGCACAGGGACTTCAAGGATG   1871

Query  398   TTGAAGCCGCCTTGCATGCCATGAAGAACGTGGCCCAGCTCATCAACGAGCGGAAGCGGA   457
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1872  TTGAAGCCGCCTTGCATGCCATGAAGAACGTGGCCCAGCTCATCAACGAGCGGAAGCGGA   1931

Query  458   GA   459
             ||
Sbjct  1932  GA   1933
```

CPU time: 0.01 user secs.   0.01 sys. secs   0.02 total secs.

Lambda   K   H
   1.33   0.621   1.12

Gapped
Lambda   K   H
   1.33   0.621   1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 146
Number of extensions: 5
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 459
Length of database: 18,725,440,322
Length adjustment: 26
Effective length of query: 433
Effective length of database: 18,725,440,296
Effective search space: 8108115648168
Effective search space used: 8108115648168
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 14 (27.6 bits)
S2: 21 (41.1 bits)